Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): An isolated compound which inhibits pilus assembly, said compound comprising a mimic of a chaperone G_1 beta-strand or a mimic of an amino terminal motif of a pilus subunit, **wherein the mimic is** ~~**with at least two alternating hydrophobic amino acid residues, or**~~ a 10 to 20 residue peptide according to formula (I):

(I) Z_1~Z_2-X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-Z_3~Z_4

or a pharmaceutically-acceptable salt thereof, wherein:

Z_1 is R-C(O)-NR- or RRN-;

Z_2 is an optional 1 to 5 residue peptide ~~**or peptide analog**~~**, 1 to 5 residue peptide analog, or 1 to 5 residues consisting of both peptide and peptide analog residues**;

X_1 is any amino acid residue;

X_2 is any amino acid residue;

X_3 is a hydrophobic residue or a hydroxyl-substituted aliphatic residue;

X_4 is any amino acid residue;

X_5 is a hydrophobic residue or Gly;

X_6 is a hydrophobic or a hydrophilic residue;

X_7 is Gly, an amide-substituted polar residue or a hydrophobic residue;

X_8 is ~~**any**~~ **an** amino acid residue **other than an aliphatic residue**;

X_9 is an aliphatic residue;

X_{10} is any amino acid residue;

Z_3 is an optional 1 to 5 residue peptide ~~or peptide analog~~, **1 to 5 residue peptide analog, or 1 to 5 residues consisting of both peptide and peptide analog residues**;

Z_4 is –C(O)OR or –C(O)NRR;

each R is independently hydrogen, $(C_1\text{-}C_6)$ alkyl, $(C_2\text{-}C_6)$ alkenyl, $(C_2\text{-}C_6)$ alkynyl or $(C_6\text{-}C_{14})$ aryl;

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and

each "~" represents a bond.

Claim 2 (original): The compound of claim 1 wherein the compound is a peptide.

Claim 3 (cancelled)

Claim 4 (currently amended): The compound of claim 1 wherein the **compound** ~~mimic comprises a mimic of a chaperone G_1 beta-strand with at least two alternating hydrophobic amino acid residues which~~ exhibits antibacterial activity against a Gram-negative bacterium.

Claim 5 (currently amended): The compound of claim 4 wherein said mimic ~~further~~ comprises ~~the amino acid sequence NVLQIAL (SEQ ID NO: 1)~~ **SEQ ID NO: 1** or an analog~~ue~~ thereof.

Claim 6 (cancelled)

Claim 7 (cancelled)

Claim 8 (currently amended): The compound of claim 1 wherein the **compound** ~~**mimic**~~ comprises a mimic of an amino terminal motif of a pilus subunit selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 9 (currently amended): The compound of claim 8 wherein said mimic of an amino-terminal motif of a pilus subunit further comprises the amino acid sequence SDVAFRGNLL (SEQ ID NO: 12) or an analog~~ue~~ thereof.

Claim 10 (cancelled)

Claim 11 (cancelled):

Claim 12 (cancelled)

Claim 13 (currently amended): The compound of claim **1** ~~**12 wherein said compound further comprises one or more features selected from the group consisting of**~~ **wherein one or more of the following conditions are satisfied**:

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 is an amide linkage;

Z_1 is H_2N–;

Z_4 is –C(O)OH or a salt thereof;

optional Z_2 is not present;

optional Z_3 is not present;

X_1 is **an amino acid residue** other than a basic residue;

X_2 is **an amino acid residue** other than an aliphatic residue;

X_3 is an aliphatic residue or T;

X_4 is **an amino acid residue** other than an acidic residue;

X_5 is an aliphatic residue, F or G;

X_7 is G, N or A; **or**

~~X_8 is other than an aliphatic residue; and~~

X_{10} is an aliphatic or a polar residue.

Claim 14 (currently amended): The compound of claim 13 ~~which is~~ **wherein the mimic comprises a sequence** selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 15 (cancelled):

Claim 16 (currently amended): **An isolated compound which inhibits pilus assembly, the compound comprising a mimic of a chaperone G_1 beta-strand or a mimic of an amino terminal motif of a pilus subunit, wherein the mimic** ~~The antibacterial compound of claim 1 which~~ is a 7 to 17 residue peptide or peptide analog according to formula (II):

(II) Z_{11}~Z_{12}–X_{11}–X_{12}–X_{13}–X_{14}–X_{15}–X_{16}–X_{17}–Z_{13}~Z_{14}

or a pharmaceutically-acceptable salt thereof, wherein:

Z_{11} is R'–C(O)–NR'– or R'R'N–;

Z_{12} is an optional 1 to 5 residue peptide ~~or peptide analog~~, **1 to 5 residue peptide analog, or 1 to 5 residues consisting of both peptide and peptide analog residues**;

X_{11} is any amino acid residue;

X_{12} is any amino acid residue;

X_{13} is a hydrophobic residue;

X_{14} is any amino acid residue;

X_{15} is a hydrophobic residue;

X_{16} is any amino acid residue;

X_{17} is hydrophobic residue or a hydroxyl-substituted aliphatic residue;

Z_{13} is an optional 1 to 5 residue peptide ~~or peptide analog, 1 to 5~~ **residue peptide analog, or 1 to 5 residues consisting of both peptide and peptide analog residues**;

Z_{14} is –C(O)OR' or –C(O)NR'R';

each R' is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl; **and**

each "–" between residues X_{11} through X_{17}, Z_{12} and X_{11} and X_{17} and Z_{13} independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and each "~" independently represents a bond.

Claim 17 (original): The compound of claim 16 ~~wherein said compound further comprises one or more features selected from the group consisting of~~ **wherein one or more of the following conditions are satisfied**:

each "–" between residues X_{11} through X_{17}, Z_{12} and X_{11} and X_{17} and Z_{13} is an amide linkage;

Z_{11} is H_2N–;

Z_{14} is –C(O)OH or a salt thereof;

optional Z_{12} is not present;

optional Z_{13} is not present;

X_{11} is **an amino acid residue** other than a basic residue;

X_{13} is an aliphatic residue or M;

X_{14} is **an amino acid residue** other than an aromatic residue;

X_{15} is an aliphatic residue, F or M; and

X_{17} is an aliphatic residue, F, M or a hydroxyl-substituted aliphatic residue.

Claim 18 (cancelled)

Claim 19 (currently amended): The compound of **any one of claims 1, 2, 5, 8, 9, 13, 14, 16, or 17** ~~**claim 16**~~ wherein said compound exhibits antibacterial activity against **one or more a** Gram-negative bacterium **selected from the group consisting of** ~~**comprising**~~ *E. coli, H. influenzae, S. euteriditis, S. typhimurium, B. pertussis, Y. pestis, Y. entarocolitica, H. pylori* and *K. pneumoniae*.

Claims 20-135 (cancelled)

Claim 136 (currently amended): **An isolated compound which inhibits pilus assembly, the compound consisting of SEQ ID NO: 12.** ~~**The compound of claim 1 wherein the compound consists of SEQ ID NO:12.**~~

Claim 137 (new): An isolated compound which inhibits pilus assembly, the compound consisting essentially of SEQ ID NO: 12, wherein the compound is a mimic of a chaperone G_1 beta-strand or a mimic of an amino terminal motif of a pilus subunit.

Claim 138 (new): An isolated compound which inhibits pilus assembly, the compound comprising a mimic of a chaperone G1 beta-strand or a mimic of an amino terminal motif of a pilus subunit, wherein the mimic comprises SEQ ID NO:12.

Claim 139 (new): The compound of claim 138 wherein the compound competitively binds to a pilus subunit hydrophobic groove.

Claim 140 (new): A complex comprising a pilus subunit with a hydrophobic groove and a synthetic compound bound thereto; the synthetic compound competitively binding the hydrophobic groove and inhibiting pilus assembly; the synthetic compound comprising a mimic of a chaperone G1 beta-strand or a mimic of an amino terminal motif of a pilus subunit; the mimic comprising at least two independently selected hydrophobic amino acid residues; and the hydrophobic amino acid residues separated by at least one interposing independently selected amino acid; wherein the hydrophobic amino acid residues facilitate binding with the hydrophobic groove of the pilus subunit.

Claim 141 (new): The complex of claim 140 wherein the synthetic compound is any one compound of claims 1, 2, 4, 5, 8, 9, 13, 14, 16, 17, 19, or 136-139.

Claim 142 (new): The complex of claim 140 wherein the mimic comprises at least three independently selected hydrophobic amino acid residues, the hydrophobic amino acid residues separated by at least one interposing independently selected amino acid.

Claim 143 (new): The complex of claim 140 wherein the mimic comprises at least four independently selected hydrophobic amino acid residues, the hydrophobic amino acid residues separated by at least one interposing independently selected amino acid.

Claim 144 (new): The complex of claim 140 wherein the mimic comprises at least five independently selected hydrophobic amino acid residues, the hydrophobic amino acid residues separated by at least one interposing independently selected amino acid.

Claim 145 (new): The complex of claim 140 wherein at least one interposing amino acid residue is an interposing hydrophobic amino acid residue.

Claim 146 (new): The complex of claim 145 with at least two interposing hydrophobic amino acid residues.

Claim 147 (new): The complex of claim 140 wherein the mimic comprises at least five consecutive hydrophobic amino acid residues.

Claim 148 (new): The complex of claim 140 wherein the mimic comprises a core sequence derived from a chaperone G_1 beta-strand or an amino terminal motif of a pilus subunit, the core sequence comprising about 3 to about 12 residues.

Claim 149 (new): The complex of claim 148 wherein the core sequence comprises about 4 to about 9 residues.

Claim 150 (new): The complex of claim 148 wherein the core sequence comprises about 7 residues.

Claim 151 (new): The complex of claim 148 wherein the core sequence is at least about 90% identical to a sequence from a chaperone G_1 beta-strand or an amino terminal motif of a pilus subunit.

Claim 152 (new): The complex of claim 148 wherein the core sequence is at least about 80% identical to a sequence from a chaperone G_1 beta-strand or an amino terminal motif of a pilus subunit.

Claim 153 (new): The complex of claim 148 wherein the core sequence is at least about 70% identical to a sequence from a chaperone G_1 beta-strand or an amino terminal motif of a pilus subunit.

Claim 154 (new): The complex of claim 140 wherein the compound exhibits antibacterial activity against a Gram-negative bacterium.

Claim 155 (new): The complex of claim 140 wherein the mimic comprises SEQ ID NO: 1 or an analog thereof.

Claim 156 (new): The complex of claim 140 wherein the mimic comprises SEQ ID NO: 12 or an analog thereof.

Claim 157 (new): The complex of claim 140 wherein the mimic comprises a sequence at least about 80% identical to a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 158 (new): The complex of any one of claims 140, 142-157 wherein the compound exhibits antibacterial activity against one or more Gram-negative bacterium selected from the group consisting of *Escherichia coli, Haemophilus influenzae, Salmonella enteriditis, Salmonella typhimurium, Bordetella pertussis, Yersinia pestis, Yersinia enterocolitica, Helicobacter pylori* and *Klebsiella pneumoniae*.